0400 #3

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/046,649

DATE: 02/07/2002
TIME: 11:08:26

Input Set : N:\Crf3\RULE60\10046649.raw
Output Set: N:\CRF3\02072002\J046649.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Young, Richard S.

(ii) TITLE OF INVENTION: Stress Proteins and Uses Therefor

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

(B) STREET: 2 Militia Drive

(C) CITY: Lexington

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02173

ENTERED

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

C--> **(A) APPLICATION NUMBER: US/10/046,649**

C--> **(B) FILING DATE: 14-Jan-2002**

(C) CLASSIFICATION: 435

C--> **(vii) PRIOR APPLICATION DATA:**

(A) APPLICATION NUMBER: 08/336,251

(B) FILING DATE:

(A) APPLICATION NUMBER: US 08/073,381

(B) FILING DATE: 04-JUN-1993

(A) APPLICATION NUMBER: US 07/804,632

(B) FILING DATE: 09-DEC-1991

(A) APPLICATION NUMBER: US 07/366,581

(B) FILING DATE: 15-JUN-1989

(A) APPLICATION NUMBER: US 07/207,298

(B) FILING DATE: 15-JUN-1988

(A) APPLICATION NUMBER: PCT/US89/02619

(B) FILING DATE: 15-JUN-1989

C--> **(viii) ATTORNEY/AGENT INFORMATION:**

(A) NAME: Granahan, Patricia

(B) REGISTRATION NUMBER: 32,227

(C) REFERENCE/DOCKET NUMBER: WHI88-08AFA3

C--> **(ix) TELECOMMUNICATION INFORMATION:**

(A) TELEPHONE: (617) 861-6240

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 amino acids

RAW SEQUENCE LISTING DATE: 02/07/2002
PATENT APPLICATION: US/10/046,649 TIME: 11:08:26

Input Set : N:\Crf3\RULE60\10046649.raw
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(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
1               5                  10                  15
Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
            20                  25                  30
Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
        35                  40                  45
Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
    50                  55                  60
Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
65                  70                  75                  80
Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
                85                  90                  95
Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
            100                 105                 110
Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
        115                 120                 125
Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
    130                 135                 140
Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
145                 150                 155                 160
Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
                165                 170                 175
Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
            180                 185                 190
Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
        195                 200                 205
Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
    210                 215                 220
Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
225                 230                 235                 240
Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
                245                 250                 255
Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
            260                 265                 270
Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
        275                 280                 285
Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
    290                 295                 300
Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
305                 310                 315                 320
Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
                325                 330                 335
Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
            340                 345                 350
Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
```

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Output Set: N:\CRF3\02072002\J046649.raw

```
149              355                 360                 365
151      Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
152          370                 375                 380
154      Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
155      385                 390                 395                 400
157      Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
158                      405                 410                 415
160      Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
161                  420                 425                 430
163      Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
164              435                 440                 445
166      Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
167          450                 455                 460
169      Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
170      465                 470                 475                 480
172      Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
173                      485                 490                 495
175      Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
176                  500                 505                 510
178      Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
179              515                 520                 525
181      Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
182          530                 535                 540
184      Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
185      545                 550                 555                 560
187      Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
188                      565                 570
190 (2) INFORMATION FOR SEQ ID NO: 2:
192      (i) SEQUENCE CHARACTERISTICS:
193           (A) LENGTH: 547 amino acids
194           (B) TYPE: amino acid
195           (D) TOPOLOGY: linear
197     (ii) MOLECULE TYPE: protein
201     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
203      Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
204      1               5                  10                  15
207      Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
208                  20                  25                  30
210      Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
211              35                  40                  45
213      Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Pro Glu Asp
214          50                  55                  60
216      Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
217      65                  70                  75                  80
219      Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
220                      85                  90                  95
223      Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
224                  100                 105                 110
226      Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
```

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```
227                115                 120                 125
229     Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
230         130                 135                 140
232     Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
233     145                 150                 155                 160
235     Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
236                     165                 170                 175
238     Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
239                 180                 185                 190
241     Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
242             195                 200                 205
244     Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
245         210                 215                 220
248     Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
249     225                 230                 235                 240
251     Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
252                     245                 250                 255
254     Glu Ala Leu Ala Thr Ala Val Val Asn Thr Ile Arg Gly Ile Val Lys
255                 260                 265                 270
257     Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
258             275                 280                 285
260     Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
261         290                 295                 300
263     Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
264     305                 310                 315                 320
266     Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
267                     325                 330                 335
269     Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
270                 340                 345                 350
272     Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
273             355                 360                 365
275     Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
276         370                 375                 380
278     Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
279     385                 390                 395                 400
281     His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
282                     405                 410                 415
284     Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln
285                 420                 425                 430
287     Asn Glu Asp Gln Asn Val Val Ser Ser Ser Leu Arg Ala Met Glu Ala
288             435                 440                 445
290     Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val Val
291         450                 455                 460
293     Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala Ala
294     465                 470                 475                 480
296     Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro Thr
297                     485                 490                 495
299     Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly Leu
300                 500                 505                 510
```

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Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp Ala
515 520 525
Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met Gly
530 535 540
Gly Met Met
545

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
1 5 10 15
Arg Gly Leu Asn Ser Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
20 25 30
Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
35 40 45
Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
50 55 60
Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
65 70 75 80
Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
85 90 95
Ala Leu Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
100 105 110
Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Lys Val Thr Glu
115 120 125
Thr Leu Leu Lys Asp Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala
130 135 140
Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
145 150 155 160
Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
165 170 175
Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
180 185 190
Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg
195 200 205
Gln Glu Ala Val Leu Glu Glu Pro Tyr Ile Leu Leu Val Ser Ser Lys
210 215 220
Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln
225 230 235 240
Ala Gly Lys Ser Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
245 250 255
Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
260 265 270
Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
275 280 285

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/046,649

DATE: 02/07/2002
TIME: 11:08:27

Input Set : N:\Crf3\RULE60\10046649.raw
Output Set: N:\CRF3\02072002\J046649.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:41 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:45 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:49 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:53 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:57 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:62 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]